GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:17:57 ; Search time 238 Seconds
                                             (without alignments)
                                             1109.272 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagttag..........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4240741 seqs, 1941225641 residues

Total number of hits satisfying chosen parameters: 8481482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	68	6	US-10-534-978A-2	Sequence 2, Appli
c 2	55.4	81.5	210920	6	US-10-540-898-99	Sequence 99, Appl
3	54.8	80.6	1000	8	US-11-266-748A-283486	Sequence 283486,
c 4	54.8	80.6	1000	8	US-11-266-748A-310126	Sequence 310126,
5	54.8	80.6	1000	8	US-11-266-748A-393223	Sequence 393223,
c 6	54.8	80.6	1000	8	US-11-266-748A-483941	Sequence 483941,

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:16:49 ; Search time 1548 Seconds
                                             (without alignments)
                                             539.767 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagttag.........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
            1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
            2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
            3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
            4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
            5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
            6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
            7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
            8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
            9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
           10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
           11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
           12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
           13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
           14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
           15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
           16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   62   91.2   62   8   US-10-712-672-5573   Sequence 5573, Ap

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:13:10 ; Search time 162 Seconds
                                    (without alignments)
                                    785.404 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagttag...........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
          1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
          2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
          3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
          4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
          5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
          6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
          7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
          8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
          9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
          10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	62	91.2	62	2	US-08-632-662A-19	Sequence 19, Appl
2	62	91.2	62	2	US-08-482-132A-14	Sequence 14, Appl
3	62	91.2	62	2	US-08-631-554A-19	Sequence 19, Appl
4	62	91.2	62	2	US-09-100-153-19	Sequence 19, Appl
5	60.4	88.8	62	3	US-08-974-549A-619	Sequence 619, App
6	60.4	88.8	62	3	US-08-912-951-329	Sequence 329, App
7	60.4	88.8	62	3	US-09-402-181B-619	Sequence 619, App

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:28:57 ; Search time 5212 Seconds
                                          (without alignments)
                                          809.438 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagttag..........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
c	1	57.2	84.1	430	18	DX787013	DX787013 2687890 V
c	2	56.8	83.5	975	18	CW924439	CW924439 EDCB443TR
c	3	56.4	82.9	471	15	AZ775262	AZ775262 2M0007D01
c	4	56.4	82.9	934	19	CR113335	CR113335 Forward s
c	5	56.2	82.6	550	3	BI786967	BI786967 sai55e09.
	6	56.2	82.6	1039	19	CNS02UID	AL214510 Tetraodon
	7	56.2	82.6	1055	19	CNS02VFA	AL215695 Tetraodon
	8	56	82.4	278	16	BZ230619	BZ230619 CH230-426
c	9	56	82.4	412	17	CE481345	CE481345 tigr-gss-
c	10	56	82.4	617	16	CE125880	CE125880 tigr-gss-
c	11	56	82.4	940	18	DU752273	DU752273 ASNF2495.
c	12	55.8	82.1	250	17	CE822593	CE822593 tigr-gss-
c	13	55.8	82.1	752	19	CNS0525K	AL317729 Tetraodon
c	14	55.8	82.1	936	18	DU760955	DU760955 ASNG3439.
	15	55.6	81.8	99	3	BJ014554	BJ014554 BJ014554
c	16	55.6	81.8	226	17	CE266979	CE266979 tigr-gss-
c	17	55.6	81.8	354	17	CW625529	CW625529 Ggal_34_U
c	18	55.6	81.8	497	18	DX794125	DX794125 2629234 V
c	19	55.6	81.8	500	18	DX766113	DX766113 2700494 V
c	20	55.6	81.8	578	19	LBAF055E09	BX541447 Leishmani
c	21	55.6	81.8	937	18	DU745259	DU745259 ASNC2695.
c	22	55.6	81.8	994	18	DU737833	DU737833 APKI4419.
c	23	55.4	81.5	87	18	DX773541	DX773541 2638389 V
c	24	55.4	81.5	151	15	AZ213114	AZ213114 Sheared D
c	25	55.4	81.5	153	17	CE606025	CE606025 tigr-gss-
c	26	55.4	81.5	165	18	DX655407	DX655407 2275293 V
c	27	55.4	81.5	166	18	DX779785	DX779785 2568866 V
c	28	55.4	81.5	171	17	CE806145	CE806145 tigr-gss-
c	29	55.4	81.5	175	16	CE041073	CE041073 tigr-gss-
c	30	55.4	81.5	181	17	CE383249	CE383249 tigr-gss-
c	31	55.4	81.5	189	18	DX766901	DX766901 2569194 V
c	32	55.4	81.5	203	16	CE181028	CE181028 tigr-gss-
c	33	55.4	81.5	206	17	CE285245	CE285245 tigr-gss-
c	34	55.4	81.5	212	18	DX959239	DX959239 CHORI105-
c	35	55.4	81.5	215	18	DX938281	DX938281 CHORI105-
c	36	55.4	81.5	216	18	DX646671	DX646671 2261399 V
c	37	55.4	81.5	217	17	CE560550	CE560550 tigr-gss-
c	38	55.4	81.5	219	16	CE166161	CE166161 tigr-gss-
c	39	55.4	81.5	242	17	CE824278	CE824278 tigr-gss-
c	40	55.4	81.5	253	17	CE503885	CE503885 tigr-gss-
c	41	55.4	81.5	260	17	CE249756	CE249756 tigr-gss-
c	42	55.4	81.5	266	17	CE462746	CE462746 tigr-gss-
c	43	55.4	81.5	281	18	DX770418	DX770418 2263546 V
c	44	55.4	81.5	286	18	DX722396	DX722396 2312598 V
c	45	55.4	81.5	290	15	AQ948278	AQ948278 Sheared D
c	46	55.4	81.5	299	17	CE513787	CE513787 tigr-gss-
c	47	55.4	81.5	303	18	DX777808	DX777808 2632848 V
c	48	55.4	81.5	314	16	CE169776	CE169776 tigr-gss-
c	49	55.4	81.5	322	18	DX789839	DX789839 2628394 V
c	50	55.4	81.5	324	18	DX765215	DX765215 2661801 V
c	51	55.4	81.5	326	16	CE056399	CE056399 tigr-gss-
c	52	55.4	81.5	329	18	DX795742	DX795742 2690845 V
c	53	55.4	81.5	332	16	CE005651	CE005651 tigr-gss-
c	54	55.4	81.5	337	18	DX680285	DX680285 2434812 V
c	55	55.4	81.5	345	18	DX791550	DX791550 2690054 V

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:09:00 ; Search time 565 Seconds
                                            (without alignments)
                                            891.891 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagttag..........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
  No.   Score   Match Length DB ID   Description
----
    1   68   100.0   68   6   ABK10341   Abk10341 Zinc fing

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:15:44 ; Search time 2750
Seconds
                                        (without alignments)
                                        1709.156 Million cell
updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1
aatccgtcgagcagagttag..........agggttagggttagggttag 68

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                1: gb_env:*
                2: gb_pat:*
                3: gb_ph:*
                4: gb_pl:*
                5: gb_pr:*
                6: gb_ro:*
                7: gb_sts:*
                8: gb_sy:*
                9: gb_un:*
                10: gb_vi:*
                11: gb_ov:*
                12: gb_htg:*
                13: gb_in:*
                14: gb_om:*
                15: gb_ba:*

     Pred. No. is the number of results predicted by chance to
have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                        SUMMARIES
     %

```
Result        Query
   No.  Score  Match Length DB   ID
Description
 --------------------------------------------------------------
-----------
      1     68  100.0    68   2   CQ818437
CQ818437 Sequence
      2     68  100.0    68   2   AX395585
AX395585 Sequence
      3     62   91.2    62   2   AR037864
AR037864 Sequence
      4     62   91.2    62   2   AR054745
AR054745 Sequence
      5     62   91.2    62   2   AR069397
AR069397 Sequence
      6     62   91.2    62   2   AX395632
AX395632 Sequence
      7   60.4   88.8    62   2   AX810663
AX810663 Sequence
      8   60.4   88.8    62   2   BD011314
BD011314 Human tel
      9   60.4   88.8    62   2   AR243525
AR243525 Sequence
     10   60.4   88.8    62   2   E37063                      E37063
Human telom
     11   60.4   88.8    62   2   AR390731
AR390731 Sequence
     12   60.4   88.8    62   2   AR393345
AR393345 Sequence
 c  13     59   86.8 202030  12   AC112339
AC112339 Rattus no
 c  14     59   86.8 301416  12   AC120690
AC120690 Rattus no
    15   58.8   86.5 257941  12   AC131474
AC131474 Rattus no
    16   58.4   85.9 124032  12   AC182354
AC182354 Loxodonta
    17   58.4   85.9 185017  12   AC130953
AC130953 Rattus no
    18   58.4   85.9 212491   6   AC105470
AC105470 Rattus no
 c  19   58.4   85.9 257714  12   AC096219
AC096219 Rattus no
    20   58.2   85.6 191168  12   AC099193
AC099193 Rattus no
 c  21   58.2   85.6 260648  12   AC117966
AC117966 Rattus no
 c  22     58   85.3  37174   4   AC151924
AC151924 Phaeodact
 c  23   57.2   84.1    148   2   AR171834
AR171834 Sequence
 c  24   57.2   84.1    148   2   AR351437
AR351437 Sequence
 c  25   57.2   84.1    148   2   I95605                      I95605
Sequence 20
 c  26   57.2   84.1 110000  12   AC110838_1
Continuation (2 of
```